```
CGCGTCCGGGCAGATTCACGTCGTTTCCAGCCAAGTGGACCTGATCGATGGCCCTCCTGAATTTATCACGATATTTGAT
TTATTAGCGATGCCCCCTGGTTTGTGTGTTACGCACACACACGTGCACACAAGGCTCTGGCTCGCTTCCCTCCCTCGTT
TCCAGCTCCTGGGCGAATCCCACATCTGTTTCAACTCTCCGCCGAGGGCGAGCAGGAGCGAGAGTGTGTCGAATCTGCG
AGTGAAGAGGGACGAGGGAAAAGAAACAAAGCCACAGACGCAACTTGAGACTCCCGCATCCCAAAAGAAGCACCAGATC

                        M   G   P   P   S   L   V   L   C   L   L   S   A   T   V   F     16
AGCAAAAAAAGAAG ATG GGC CCC CCG AGC CTC GTG CTG TGC TTG CTG TCC GCA ACT GTG TTC     48

 S   L   L   G   G   S   S   A   F   L   S   H   H   R   L   K   G   R   F   Q     36
TCC CTG CTG GGT GGA AGC TCG GCC TTC CTG TCG CAC CAC CGC CTG AAA GGC AGG TTT CAG   108

 R   D   R   R   N   I   R   P   N   I   I   L   V   L   T   D   D   Q   D   V     56
AGG GAC CGC AGG AAC ATC CGC CCC AAC ATC ATC CTG GTG CTG ACG GAC GAC CAG GAT GTG   168

 E   L   G   S   M   Q   V   M   N   K   T   R   R   I   M   E   Q   G   G   T     76
GAG CTG GGT TCC ATG CAG GTG ATG AAC AAG ACC CGG CGC ATC ATG GAG CAG GGC GGG ACG   228

 H   F   I   N   A   F   V   T   T   P   M   C   C   P   S   R   S   S   I   L     96
CAC TTC ATC AAC GCC TTC GTG ACC ACA CCC ATG TGC TGC CCC TCA CGC TCC TCC ATC CTC   288

 T   G   K   Y   V   H   N   H   N   T   Y   T   N   N   E   N   C   S   S   P    116
ACC GGC AAG TAC GTC CAC AAC CAC AAC ACC TAC ACC AAC AAT GAG AAC TGC TCC TCG CCC   348

 S   W   Q   A   Q   H   E   S   R   T   F   A   V   Y   L   N   S   T   G   Y    136
TCC TGG CAG GCA CAG CAC GAG AGC CGC ACC TTT GCC GTG TAC CTC AAT AGC ACT GGC TAC   408
```

Fig. 1A

R	T	A	F	F	G	K	Y	L	N	E	Y	N	G	S	Y	V	P	P	G	156
CGG	ACA	GCT	TTC	TTC	GGG	AAG	TAT	CTT	AAT	GAA	TAC	AAC	GGC	TCC	TAC	GTG	CCA	CCC	GGC	468
W	K	E	W	V	G	L	L	K	N	S	R	F	Y	N	Y	T	L	C	R	176
TGG	AAG	GAG	TGG	GTC	GGA	CTC	CTT	AAA	AAC	TCC	CGC	TTT	TAT	AAC	TAC	ACG	CTG	TGT	CGG	528
N	G	V	K	E	K	H	G	S	D	Y	S	K	D	Y	L	T	D	L	I	196
AAC	GGG	GTG	AAA	GAG	AAG	CAC	GGC	TCC	GAC	TAC	TCC	AAG	GAT	TAC	CTC	ACA	GAC	CTC	ATC	588
T	N	D	S	V	S	F	F	R	T	S	K	K	M	Y	P	H	R	P	V	216
ACC	AAT	GAC	AGC	GTG	AGC	TTC	TTC	CGC	ACG	TCC	AAG	AAG	ATG	TAC	CCG	CAC	AGG	CCA	GTC	648
L	M	V	I	S	H	A	A	P	H	G	P	E	D	S	A	P	Q	Y	S	236
CTC	ATG	GTC	ATC	AGC	CAT	GCA	GCC	CCC	CAC	GGC	CCT	GAG	GAT	TCA	GCC	CCA	CAA	TAT	TCA	708
R	L	F	P	N	A	S	Q	H	I	T	P	S	Y	N	Y	A	P	N	P	256
CGC	CTC	TTC	CCA	AAC	GCA	TCT	CAG	CAC	ATC	ACG	CCG	AGC	TAC	AAC	TAC	GCG	CCC	AAC	CCG	768
D	K	H	W	I	M	R	Y	T	G	P	M	K	P	I	H	M	E	F	T	276
GAC	AAA	CAC	TGG	ATC	ATG	CGC	TAC	ACG	GGG	CCC	ATG	AAG	CCC	ATC	CAC	ATG	GAA	TTC	ACC	828
N	M	L	Q	R	K	R	L	Q	T	L	M	S	V	D	D	S	M	E	T	296
AAC	ATG	CTC	CAG	CGG	AAG	CGC	TTG	CAG	ACC	CTC	ATG	TCG	GTG	GAC	GAC	TCC	ATG	GAG	ACG	888
I	Y	N	M	L	V	E	T	G	E	L	D	N	T	Y	I	V	Y	T	A	316
ATT	TAC	AAC	ATG	CTG	GTT	GAG	ACG	GGC	GAG	CTG	GAC	AAC	ACG	TAC	ATC	GTA	TAC	ACC	GCC	948

Fig. 1B

```
 D   H   G   Y   H   I   G   Q   F   G   L   V   K   G   K   S   M   P   Y   E   336
GAC CAC GGT TAC CAC ATC GGC CAG TTT GGC CTG GTG AAA GGG AAA TCC ATG CCA TAT GAG 1008

 F   D   I   R   V   P   F   Y   V   R   G   P   N   V   E   A   G   C   L   N   356
TTT GAC ATC AGG GTC CCG TTC TAC GTG AGG GGC CCC AAC GTG GAA GCC GGC TGT CTG AAT 1068

 P   H   I   V   L   N   I   D   L   A   P   T   I   L   D   I   A   G   L   D   376
CCC CAC ATC GTC CTC AAC ATT GAC CTG GCC CCC ACC ATC CTG GAC ATT GCA GGC CTG GAC 1128

 I   P   A   D   M   D   G   K   S   I   L   K   L   L   D   T   E   R   P   V   396
ATA CCT GCG GAT ATG GAC GGG AAA TCC ATC CTC AAG CTG CTG GAC ACG GAG CGG CCG GTG 1188

 N   R   F   H   L   K   K   K   M   R   V   W   R   D   S   F   L   V   E   R   416
AAT CGG TTT CAC TTG AAA AAG AAG ATG AGG GTC TGG CGG GAC TCC TTC TTG GTG GAG AGA 1248

 G   K   L   L   H   K   R   D   N   D   K   V   D   A   Q   E   E   N   F   L   436
GGC AAG CTG CTA CAC AAG AGA GAC AAT GAC AAG GTG GAC GCC CAG GAG GAG AAC TTT CTG 1308

 P   K   Y   Q   R   V   K   D   L   C   Q   R   A   E   Y   Q   T   A   C   E   456
CCC AAG TAC CAG CGT GTG AAG GAC CTG TGT CAG CGT GCT GAG TAC CAG ACG GCG TGT GAG 1368

 Q   L   G   Q   K   W   Q   C   V   E   D   A   T   G   K   L   K   L   H   K   476
CAG CTG GGA CAG AAG TGG CAG TGT GTG GAG GAC GCC ACG GGG AAG CTG AAG CTG CAT AAG 1428

 C   K   G   P   M   R   L   G   G   S   R   A   L   S   N   L   V   P   K   Y   496
TGC AAG GGC CCC ATG CGG CTG GGC GGC AGC AGA GCC CTC TCC AAC CTC GTG CCC AAG TAC 1488
```

Fig. 1C

```
                                                                    516
 Y   G   Q   G   S   E   A   C   T   C   D   S   G   D   Y   K   L   S   L   A
TAC GGG CAG GGC AGC GAG GCC TGC ACC TGT GAC AGC GGG GAC TAC AAG CTC AGC CTG GCC 1548

                                                                    536
 G   R   R   K   K   L   F   K   K   K   Y   K   A   S   Y   V   R   S   R   S
GGA CGC CGG AAA AAA CTC TTC AAG AAG AAG TAC AAG GCC AGC TAT GTC CGC AGT CGC TCC 1608

                                                                    556
 I   R   S   V   A   I   E   V   D   G   R   V   Y   H   V   G   L   G   D   A
ATC CGC TCA GTG GCC ATC GAG GTG GAC GGC AGG GTG TAC CAC GTA GGC CTG GGT GAT GCC 1668

                                                                    576
 A   Q   P   R   N   L   T   K   R   H   W   P   G   A   P   E   D   Q   D   D
GCC CAG CCC CGA AAC CTC ACC AAG CGG CAC TGG CCA GGG GCC CCT GAG GAC CAA GAT GAC 1728

                                                                    596
 K   D   G   G   D   F   S   G   T   G   G   L   P   D   Y   S   A   A   N   P
AAG GAT GGT GGG GAC TTC AGT GGC ACT GGA GGC CTT CCC GAC TAC TCA GCC GCC AAC CCC 1788

                                                                    616
 I   K   V   T   H   R   C   Y   I   L   E   N   D   T   V   Q   C   D   L   D
ATT AAA GTG ACA CAT CGG TGC TAC ATC CTA GAG AAC GAC ACA GTC CAG TGT GAC CTG GAC 1848

                                                                    636
 L   Y   K   S   L   Q   A   W   K   D   H   K   L   H   I   D   H   E   I   E
CTG TAC AAG TCC CTG CAG GCC TGG AAA GAC CAC AAG CTG CAC ATC GAC CAC GAG ATT GAA 1908

                                                                    656
 T   L   Q   N   K   I   K   N   L   R   E   V   R   G   H   L   K   K   K   R
ACC CTG CAG AAC AAA ATT AAG AAC CTG AGG GAA GTC CGA GGT CAC CTG AAG AAA AAG CGG 1968

                                                                    676
 P   E   E   C   D   C   H   K   I   S   Y   H   T   Q   H   K   G   R   L   K
CCA GAA GAA TGT GAC TGT CAC AAA ATC AGC TAC CAC ACC CAG CAC AAA GGC CGC CTC AAG 2028
```

Fig. 1D

```
H   R   G   S   S   L   H   P   F   R   K   G   L   Q   E   K   D   K   V   W   696
CAC AGA GGC TCC AGT CTG CAT CCT TTC AGG AAG GGC CTG CAA GAG AAG GAC AAG GTG TGG 2088

L   L   R   E   Q   K   R   K   K   K   L   R   K   L   L   K   R   L   Q   N   716
CTG TTG CGG GAG CAG AAG CGC AAG AAG AAA CTC CGC AAG CTG CTC AAG CGC CTG CAG AAC 2148

N   D   T   C   S   M   P   G   L   T   C   F   T   H   D   N   Q   H   W   Q   736
AAC GAC ACG TGC AGC ATG CCA GGC CTC ACG TGC TTC ACC CAC GAC AAC CAG CAC TGG CAG 2208

T   A   P   F   W   T   L   G   P   F   C   A   C   T   S   A   N   N   N   T   756
ACG GCG CCT TTC TGG ACA CTG GGG CCT TTC TGT GCC TGC ACC AGC GCC AAC AAT AAC ACG 2268

Y   W   C   M   R   T   I   N   E   T   H   N   F   L   F   C   E   F   A   T   776
TAC TGG TGC ATG AGG ACC ATC AAT GAG ACT CAC AAT TTC CTC TTC TGT GAA TTT GCA ACT 2328

G   F   L   E   Y   F   D   L   N   T   D   P   Y   Q   L   M   N   A   V   N   796
GGC TTC CTA GAG TAC TTT GAT CTC AAC ACA GAC CCC TAC CAG CTG ATG AAT GCA GTG AAC 2388

T   L   D   R   D   V   L   N   Q   L   H   V   Q   L   M   E   L   R   S   C   816
ACA CTG GAC AGG GAT GTC CTC AAC CAG CTA CAC GTA CAG CTC ATG GAG CTG AGG AGC TGC 2448

K   G   Y   K   Q   C   N   P   R   T   R   N   M   D   L   G   L   K   D   G   836
AAG GGT TAC AAG CAG TGT AAC CCC CGG ACT CGA AAC ATG GAC CTG GGA CTT AAA GAT GGA 2508

G   S   Y   E   Q   Y   R   Q   F   Q   R   R   K   W   P   E   M   K   R   P   856
GGA AGC TAT GAG CAA TAC AGG CAG TTT CAG CGT CGA AAG TGG CCA GAA ATG AAG AGA CCT 2568
```

Fig. 1E

```
                                                                    870
 S   S   K   S   L   G   Q   L   W   E   G   W   E   G   *          2613
TCT TCC AAA TCA CTG GGA CAA CTG TGG GAA GGC TGG GAA GGT TAA

GAAACAACAGAGGTGGACCTCCAAAAACATAGAGGCATCACCTGACTGCACAGGCAATGAAAAACCATGTGGGTGATTT
CCAGCAGACCTGTGCTATTGGCCAGGAGGCCTGAGAAAGCAAGCACGCACTCTCAGTCAACATGACAGATTCTGGAGGA
TAACCAGCAGGAGCAGAGATAACTTCAGGAAGTCCATTTTTGCCCCTGCTTTTGCTTTGGATTATACCTCACCAGCTGC
ACAAAATGCATTTTTTCGTATCAAAAAGTCACCACTAACCCTCCCCCAGAAGCTCACAAAGGAAAACGGAGAGAGCGAG
CGAGAGAGATTTCCTTGGAAATTTCTCCCAAGGGCGAAAGTCATTGGAATTTTTAAATCATAGGGGAAAAGCAGTCCTG
TTCTAAATCCTCTTATTCTTTTGGTTTGTCACAAAGAAGGAACTAAGAAGCAGGACAGAGGCAACGTGGAGAGGCTGAA
AACAGTGCAGAGACGTTTGACAATGAGTCAGTAGCACAAAAGAGATGACATTTACCTAGCACTATAAACCCTGGTTGCC
TCTGAAGAAACTGCCTT
```

Fig. 1F

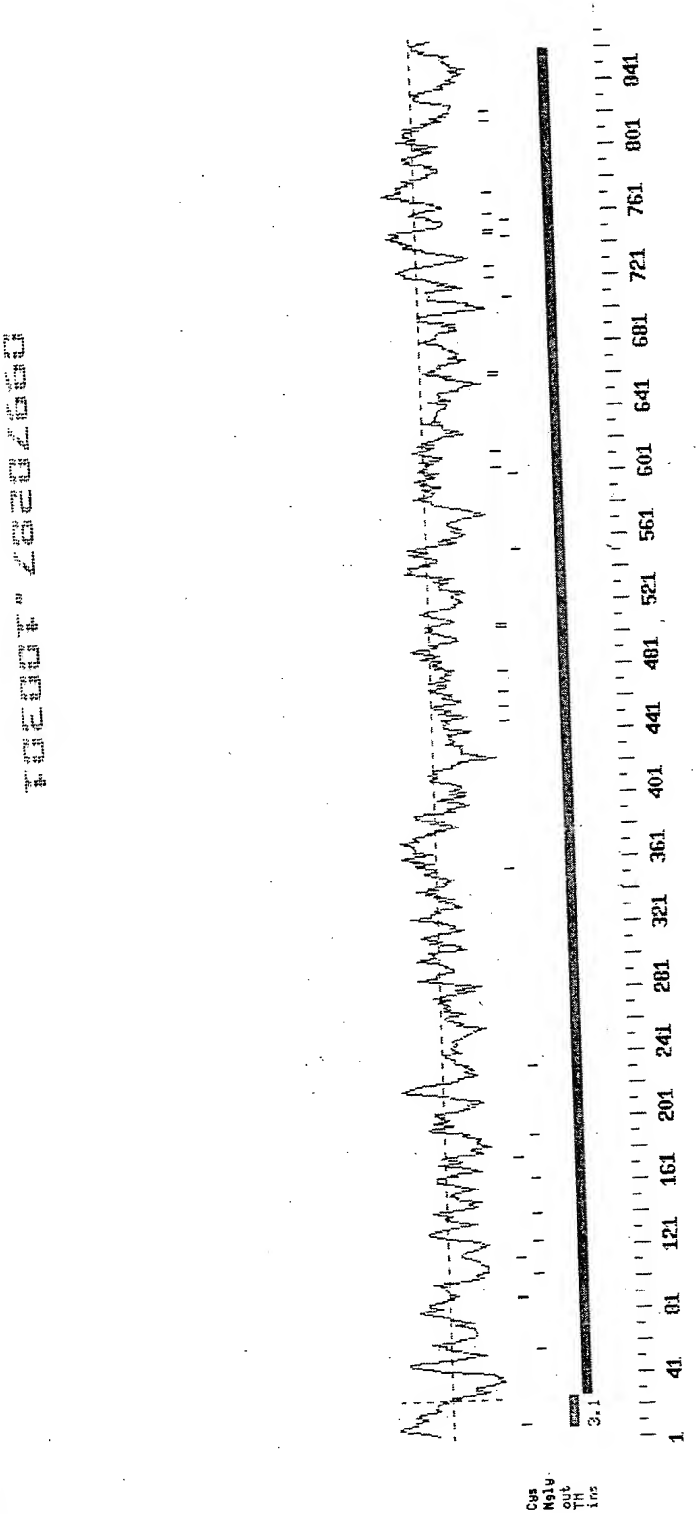
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Fig. 2

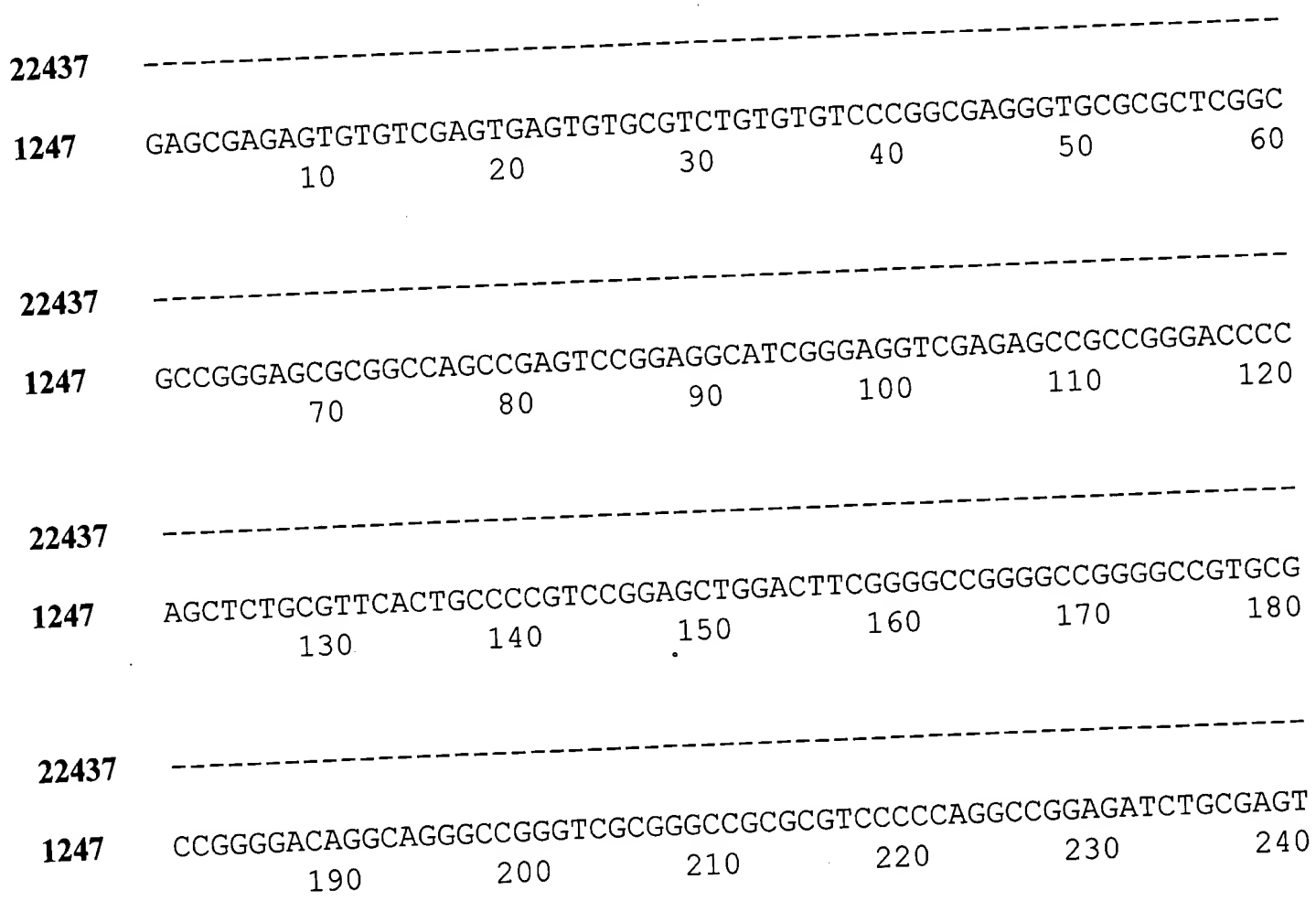

22437 ----------
1247 GAGCGAGAGTGTGTCGAGTGAGTGTGCGTCTGTGTGTCCCGGCGAGGGTGCGCGCTCGGC
10 20 30 40 50 60
22437 ----------
1247 GCCGGGAGCGCGGCCAGCCGAGTCCGGAGGCATCGGGAGGTCGAGAGCCGCCGGGACCCC
70 80 90 100 110 120
22437 ----------
1247 AGCTCTGCGTTCACTGCCCCGTCCGGAGCTGGACTTCGGGGCCGGGGCCGGGGCCGTGCG
130 140 150 160 170 180
22437 ----------
1247 CCGGGGACAGGCAGGGCCGGGTCGCGGGCCGCGCGTCCCCCAGGCCGGAGATCTGCGAGT
190 200 210 220 230 240

Fig. 3A

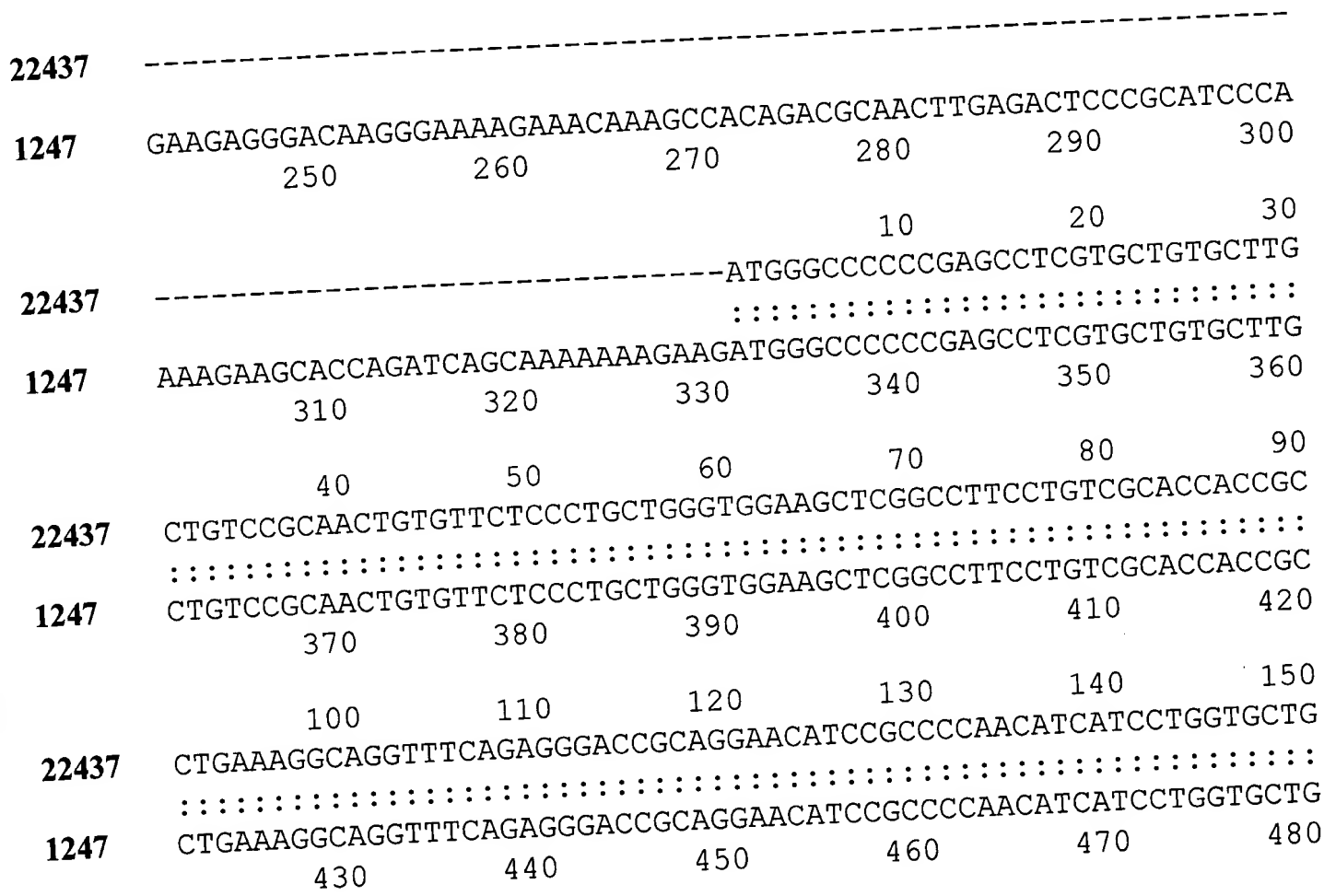


Fig. 3B

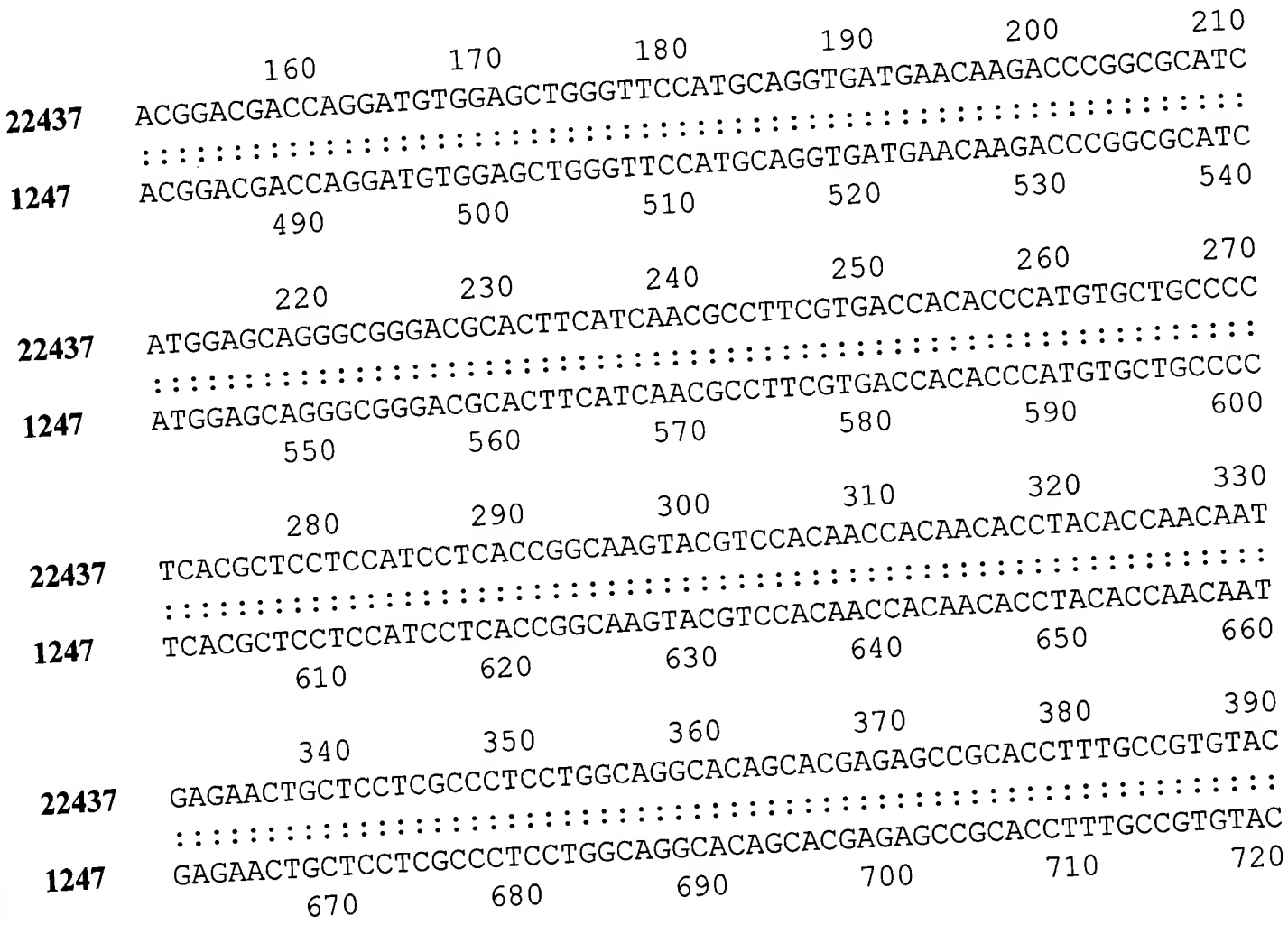

160 170 180 190 200 210
22437 ACGGACGACCAGGATGTGGAGCTGGGTTCCATGCAGGTGATGAACAAGACCCGGCGCATC
1247 ACGGACGACCAGGATGTGGAGCTGGGTTCCATGCAGGTGATGAACAAGACCCGGCGCATC
490 500 510 520 530 540
220 230 240 250 260 270
22437 ATGGAGCAGGGCGGGACGCACTTCATCAACGCCTTCGTGACCACACCCATGTGCTGCCCC
1247 ATGGAGCAGGGCGGGACGCACTTCATCAACGCCTTCGTGACCACACCCATGTGCTGCCCC
550 560 570 580 590 600
280 290 300 310 320 330
22437 TCACGCTCCTCCATCCTCACCGGCAAGTACGTCCACAACCACAACACCTACACCAACAAT
1247 TCACGCTCCTCCATCCTCACCGGCAAGTACGTCCACAACCACAACACCTACACCAACAAT
610 620 630 640 650 660
340 350 360 370 380 390
22437 GAGAACTGCTCCTCGCCCTCCTGGCAGGCACAGCACGAGAGCCGCACCTTTGCCGTGTAC
1247 GAGAACTGCTCCTCGCCCTCCTGGCAGGCACAGCACGAGAGCCGCACCTTTGCCGTGTAC
670 680 690 700 710 720

Fig. 3C

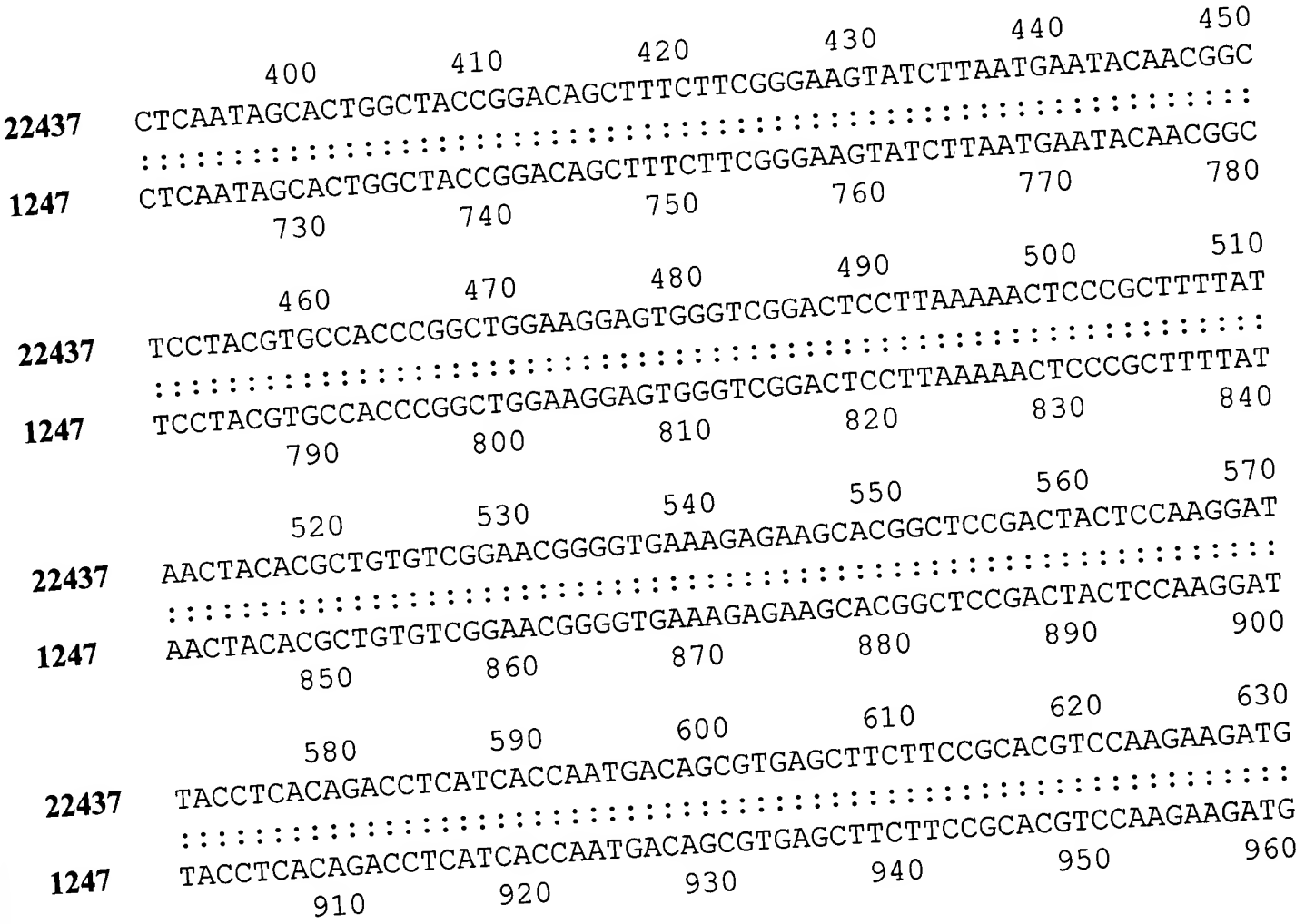


Fig. 3D

```
               640       650       660       670       680       690
22437   TACCCGCACAGGCCAGTCCTCATGGTCATCAGCCATGCAGCCCCCCACGGCCCTGAGGAT
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1247    TACCCGCACAGGCCAGTCCTCATGGTCATCAGCCATGCAGCCCCCCACGGCCCTGAGGAT
               970       980       990      1000      1010      1020

               700       710       720       730       740       750
22437   TCAGCCCCACAATATTCACGCCTCTTCCCAAACGCATCTCAGCACATCACGCCGAGCTAC
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1247    TCAGCCCCACAATATTCACGCCTCTTCCCAAACGCATCTCAGCACATCACGCCGAGCTAC
              1030      1040      1050      1060      1070      1080

               760       770       780       790       800       810
22437   AACTACGCGCCCAACCCGGACAAACACTGGATCATGCGCTACACGGGGCCCATGAAGCCC
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1247    AACTACGCGCCCAACCCGGACAAACACTGGATCATGCGCTACACGGGGCCCATGAAGCCC
              1090      1100      1110      1120      1130      1140

               820       830       840       850       860       870
22437   ATCCACATGGAATTCACCAACATGCTCCAGCGGAAGCGCTTGCAGACCCTCATGTCGGTG
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1247    ATCCACATGGAATTCACCAACATGCTCCAGCGGAAGCGCTTGCAGACCCTCATGTCGGTG
              1150      1160      1170      1180      1190      1200
```

Fig. 3E

```
                880        890        900        910        920        930
22437 GACGACTCCATGGAGACGATTTACAACATGCTGGTTGAGACGGGCGAGCTGGACAACACG
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1247  GACGACTCCATGGAGACGATTTACAACATGCTGGTTGAGACGGGCGAGCTGGACAACACG
           1210       1220       1230       1240       1250       1260

                940        950        960        970        980        990
22437 TACATCGTATACACCGCCGACCACGGTTACCACATCGGCCAGTTTGGCCTGGTGAAAGGG
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1247  TACATCGTATACACCGCCGACCACGGTTACCACATCGGCCAGTTTGGCCTGGTGAAAGGG
           1270       1280       1290       1300       1310       1320

               1000       1010       1020       1030       1040       1050
22437 AAATCCATGCCATATGAGTTTGACATCAGGGTCCCGTTCTACGTGAGGGGCCCCAACGTG
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1247  AAATCCATGCCATATGAGTTTGACATCAGGGTCCCGTTCTACGTGAGGGGCCCCAACGTG
           1330       1340       1350       1360       1370       1380

               1060       1070       1080       1090       1100       1110
22437 GAAGCCGGCTGTCTGAATCCCCACATCGTCCTCAACATTGACCTGGCCCCCACCATCCTG
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1247  GAAGCCGGCTGTCTGAATCCCCACATCGTCCTCAACATTGACCTGGCCCCCACCATCCTG
           1390       1400       1410       1420       1430       1440
```

Fig. 3F


1120 1130 1140 1150 1160 1170
22437 GACATTGCAGGCCTGGACATACCTGCGGATATGGACGGGAAATCCATCCTCAAGCTGCTG
1247 GACATTGCAGGCCTGGACATACCTGCGGATATGGACGGGAAATCCATCCTCAAGCTGCTG
1450 1460 1470 1480 1490 1500
1180 1190 1200 1210 1220 1230
22437 GACACGGAGCGGCCGGTGAATCGGTTTCACTTGAAAAAGAAGATGAGGGTCTGGCGGGAC
1247 GACACGGAGCGGCCGGTGAATCGGTTTCACTTGAAAAAGAAGATGAGGGTCTGGCGGGAC
1510 1520 1530 1540 1550 1560
1240 1250 1260 1270 1280 1290
22437 TCCTTCTTGGTGGAGAGAGGCAAGCTGCTACACAAGAGAGACAATGACAAGGTGGACGCC
1247 TCCTTCTTGGTGGAGAGAGGCAAGCTGCTACACAAGAGAGACAATGACAAGGTGGACGCC
1570 1580 1590 1600 1610 1620
1300 1310 1320 1330 1340 1350
22437 CAGGAGGAGAACTTTCTGCCCAAGTACCAGCGTGTGAAGGACCTGTGTCAGCGTGCTGAG
1247 CAGGAGGAGAACTTTCTGCCCAAGTACCAGCGTGTGAAGGACCTGTGTCAGCGTGCTGAG
1630 1640 1650 1660 1670 1680

Fig. 3G

```
                1360      1370      1380      1390      1400      1410
22437 TACCAGACGGCGTGTGAGCAGCTGGGACAGAAGTGGCAGTGTGTGGAGGACGCCACGGGG
      :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1247  TACCAGACGGCGTGTGAGCAGCTGGGACAGAAGTGGCAGTGTGTGGAGGACGCCACGGGG
         1690      1700      1710      1720      1730      1740

                1420      1430      1440      1450      1460      1470
22437 AAGCTGAAGCTGCATAAGTGCAAGGGCCCCCATGCGGCTGGGCGGCAGCAGAGCCCTCTCC
      :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1247  AAGCTGAAGCTGCATAAGTGCAAGGGCCCCCATGCGGCTGGGCGGCAGCAGAGCCCTCTCC
         1750      1760      1770      1780      1790      1800

                1480      1490      1500      1510      1520      1530
22437 AACCTCGTGCCCAAGTACTACGGGCAGGGCAGCGAGGCCTGCACCTGTGACAGCGGGGAC
      :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1247  AACCTCGTGCCCAAGTACTACGGGCAGGGCAGCGAGGCCTGCACCTGTGACAGCGGGGAC
         1810      1820      1830      1840      1850      1860

                1540      1550      1560      1570      1580      1590
22437 TACAAGCTCAGCCTGGCCGGACGCCGGAAAAAACTCTTCAAGAAGAAGTACAAGGCCAGC
      :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1247  TACAAGCTCAGCCTGGCCGGACGCCGGAAAAAACTCTTCAAGAAGAAGTACAAGGCCAGC
         1870      1880      1890      1900      1910      1920
```

Fig. 3H

```
                1600       1610       1620       1630       1640       1650
22437  TATGTCCGCAGTCGCTCCATCCGCTCAGTGGCCATCGAGGTGGACGGCAGGGTGTACCAC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1247   TATGTCCGCAGTCGCTCCATCCGCTCAGTGGCCATCGAGGTGGACGGCAGGGTGTACCAC
                1930       1940       1950       1960       1970       1980

                1660       1670       1680       1690       1700       1710
22437  GTAGGCCTGGGTGATGCCGCCCAGCCCCGAAACCTCACCAAGCGGCACTGGCCAGGGGCC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1247   GTAGGCCTGGGTGATGCCGCCCAGCCCCGAAACCTCACCAAGCGGCACTGGCCAGGGGCC
                1990       2000       2010       2020       2030       2040

                1720       1730       1740       1750       1760       1770
22437  CCTGAGGACCAAGATGACAAGGATGGTGGGGACTTCAGTGGCACTGGAGGCCTTCCCGAC
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1247   CCTGAGGACCAAGATGACAAGGATGGTGGGGACTTCAGTGGCACTGGAGGCCTTCCCGAC
                2050       2060       2070       2080       2090       2100
```

Fig. 3I

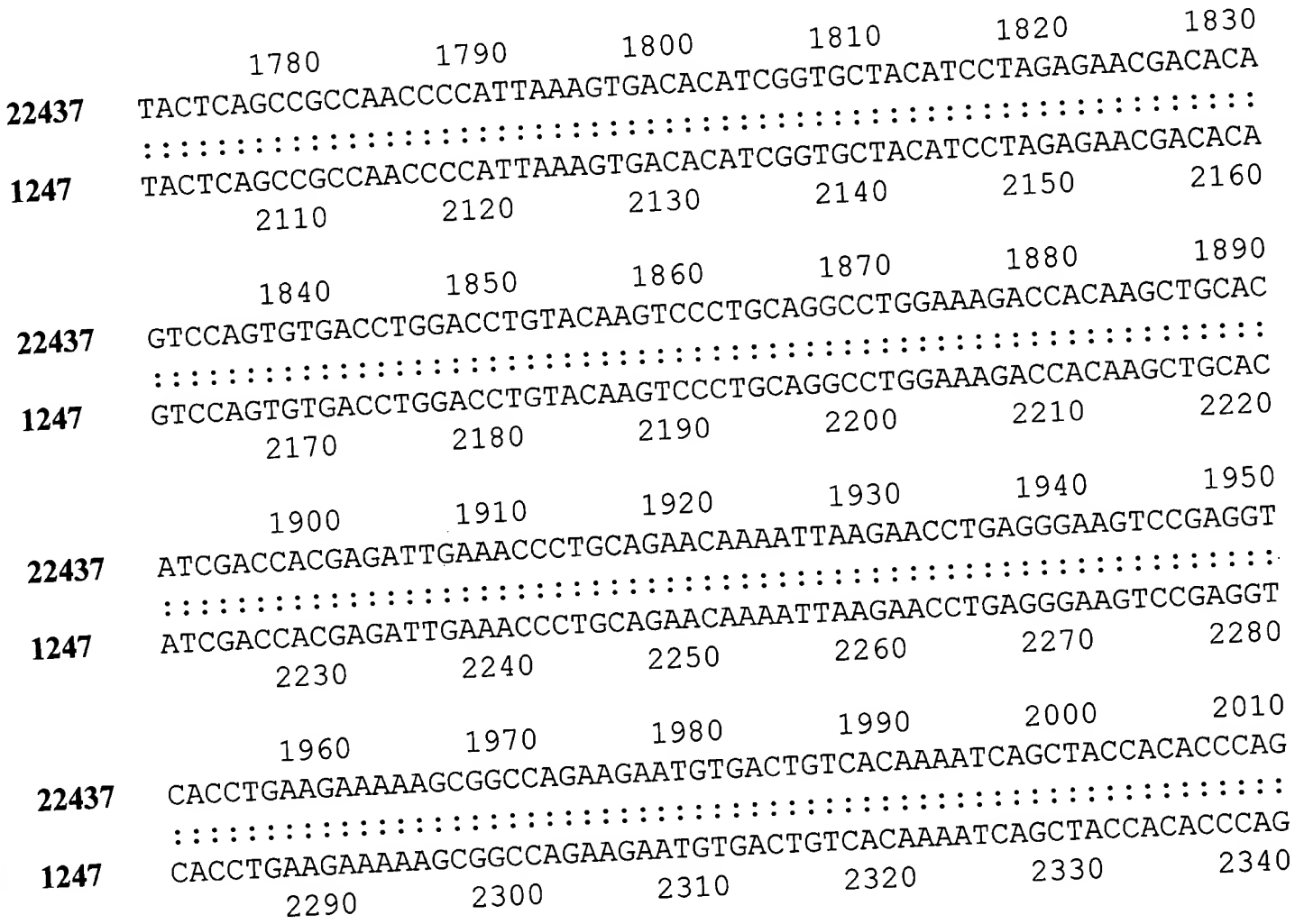


Fig. 3J

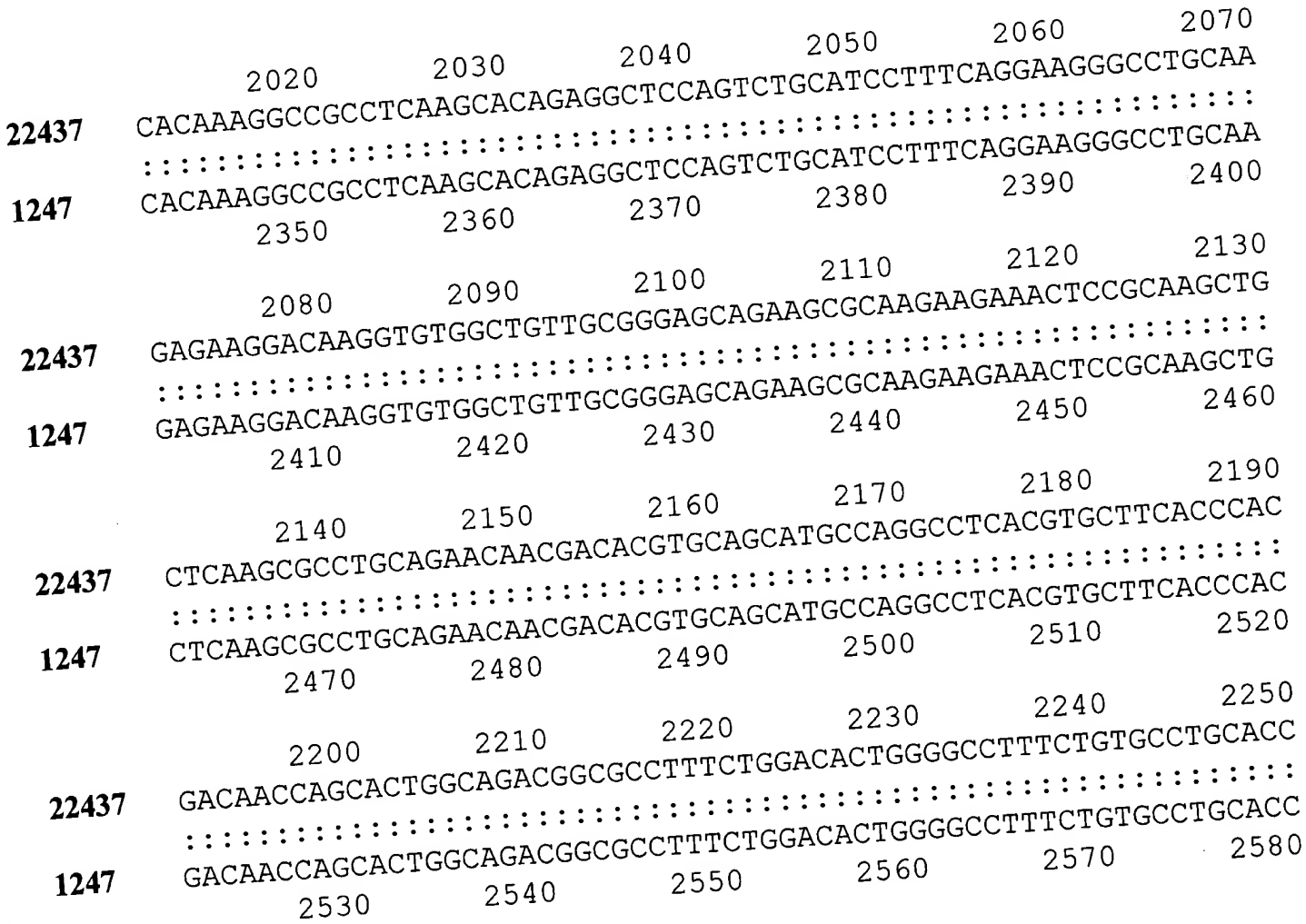


Fig. 3K

```
                2260        2270        2280        2290        2300        2310
22437 AGCGCCAACAATAACACGTACTGGTGCATGAGGACCATCAATGAGACTCACACAATTTCCTC
      :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1247  AGCGCCAACAATAACACGTACTGGTGCATGAGGACCATCAATGAGACTCACACAATTTCCTC
         2590        2600        2610        2620        2630        2640

                2320        2330        2340        2350        2360        2370
22437 TTCTGTGAATTTGCAACTGGCTTCCTAGAGTACTTTGATCTCAACACAGACCCCTACCAG
      :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1247  TTCTGTGAATTTGCAACTGGCTTCCTAGAGTACTTTGATCTCAACACAGACCCCTACCAG
         2650        2660        2670        2680        2690        2700

                2380        2390        2400        2410        2420        2430
22437 CTGATGAATGCAGTGAACACACTGGACAGGGATGTCCTCAACCAGCTACACGTACAGCTC
      :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1247  CTGATGAATGCAGTGAACACACTGGACAGGGATGTCCTCAACCAGCTACACGTACAGCTC
         2710        2720        2730        2740        2750        2760

                2440        2450        2460        2470        2480        2490
22437 ATGGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTGTAACCCCCGGACTCGAAACATGGAC
      :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1247  ATGGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTGTAACCCCCGGACTCGAAACATGGAC
         2770        2780        2790        2800        2810        2820
```

Fig. 3L

```
                2500        2510        2520        2530        2540        2550
22437 CTGGGACTTAAAGATGGAGGAAGCTATGAGCAATACAGGCAGTTTCAGCGTCGAAAGTGG
      :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1247  CTGGGACTTAAAGATGGAGGAAGCTATGAGCAATACAGGCAGTTTCAGCGTCGAAAGTGG
           2830        2840        2850        2860        2870        2880

                2560        2570        2580        2590        2600        2610
22437 CCAGAAATGAAGAGACCTTCTTCCAAATCACTGGGACAACTGTGGGAAGGCTGGGAAGGT
      :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1247  CCAGAAATGAAGAGACCTTCTTCCAAATCACTGGGACAACTGTGGGAAGGCTGGGAAGGT
           2890        2900        2910        2920        2930        2940

22437 TAA----------------------------------------------------------
      :::
1247  TAAGAAACAACAGAGGTGGACCTCCAAAAACATAGAGGCATCACCTGACTGCACAGGCAA
           2950        2960        2970        2980        2990        3000

22437 ----------------------------------------------------------------

1247  TGAAAAACCATGTGGGTGATTTCCAGCAGACCTGTGCTATTGGCCAGGAGGCCTGAGAAA
           3010        3020        3030        3040        3050        3060
```

Fig. 3M

22437 ----------

1247 GCAAGCACGCACTCTCAGTCAACATGACAGATTCTGGAGGATAACCAGCAGGAGCAGAGA
3070 3080 3090 3100 3110 3120

22437 ----------

1247 TAACTTCAGGAAGTCCATTTTTGCCCCTGCTTTTGCTTTGGATTATACCTCACCAGCTGC
3130 3140 3150 3160 3170 3180

22437 ----------

1247 ACAAAATGCATTTTTTCGTATCAAAAAGTCACCACTAACCCTCCCCCAGAAGCTCACAAA
3190 3200 3210 3220 3230 3240

22437 ----------

1247 GGAAAACGGAGAGAGCGAGCGAGAGAGATTTCCTTGGAAATTTCTCCCAAGGGCGAAAGT
3250 3260 3270 3280 3290 3300

Fig. 3N

22437 ----------

1247 CATTGGAATTTTTAAATCATAGGGGAAAAGCAGTCCTGTTCTAAATCCTCTTATTCTTTT
3310 3320 3330 3340 3350 3360

22437 ----------

1247 GGTTTGTCACAAAGAAGGAACTAAGAAGCAGGACAGAGGCAACGTGGAGAGGCTGAAAAC
3370 3380 3390 3400 3410 3420

22437 ----------

1247 AGTGCAGAGACGTTTGACAATGAGTCAGTAGCACAAAAGAGATGACATTTACCTAGCACT
3430 3440 3450 3460 3470 3480

22437 ----------

1247 ATAAACCCTGGTTGCCTCTGAAGAAACTGCCTTCATTGTATATATGTGACTATTTACATG
3490 3500 3510 3520 3530 3540

Fig. 3O


22437
1247
TAATCAACATGGGAACTTTTAGGGGAACCTAATAAGAAATCCCAATTTTCAGGAGTGGTG
3550 3560 3570 3580 3590 3600
22437
1247
GTGTCAATAAACGCTCTGTGGCCAGTGTAAAAGAAAATCCCTCGCAGTTGTGGACATTTC
3610 3620 3630 3640 3650 3660
22437
1247
TGTTCCTGTCCAGATACCATTTCTCCTAGTATTTCTTTGTTATGTCCCAGAACTGATGTT
3670 3680 3690 3700 3710 3720
22437
1247
TTTTTTTTAAGGTACTGAAAAGAAATGAAGTTGATGTATGTCCCAAGTTTTGATGAAACT
3730 3740 3750 3760 3770 3780

Fig. 3P

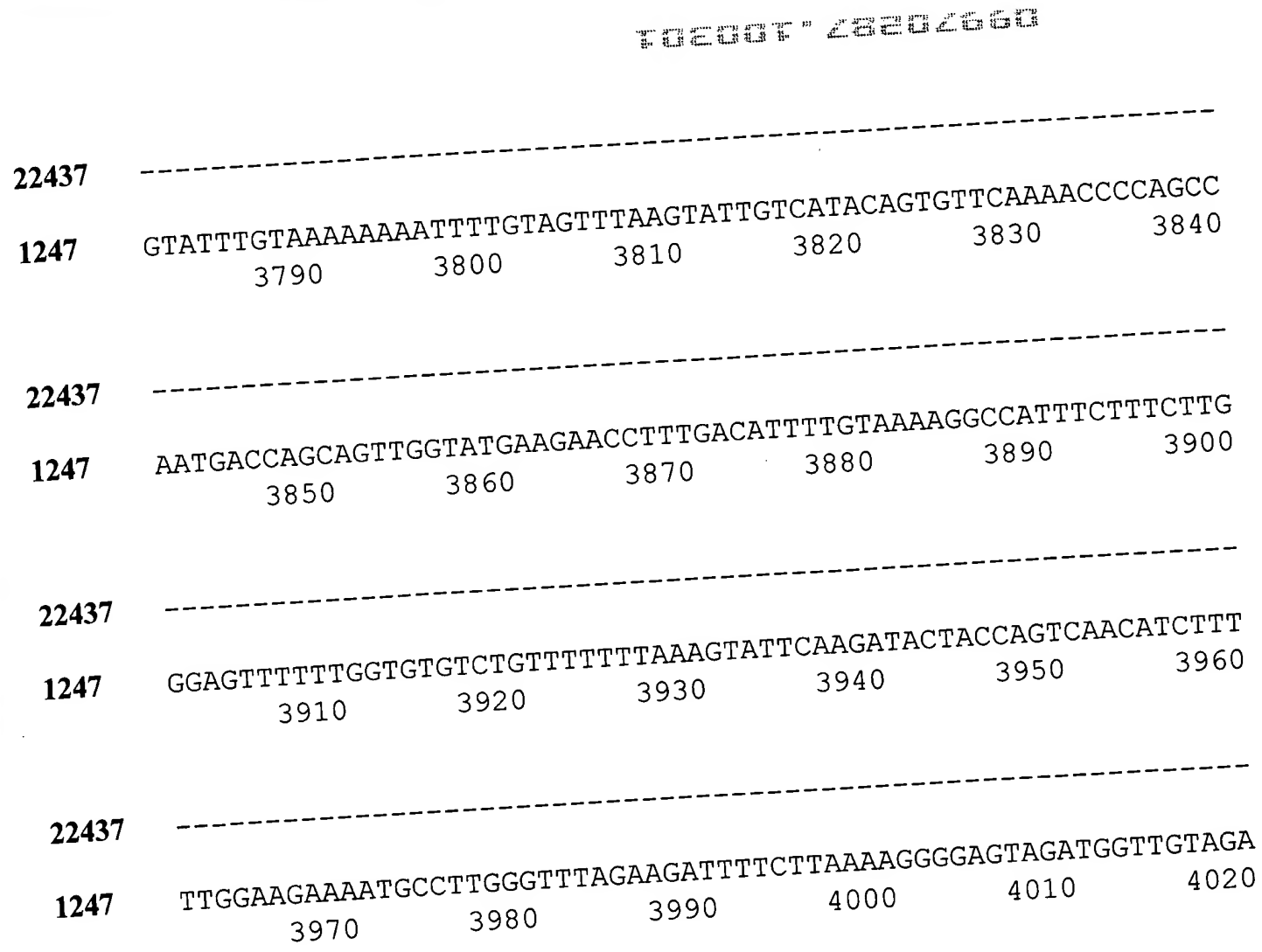

22437
1247
GTATTTGTAAAAAAAATTTTGTAGTTTAAGTATTGTCATACAGTGTTCAAAACCCCAGCC
3790 3800 3810 3820 3830 3840
22437
1247
AATGACCAGCAGTTGGTATGAAGAACCTTTGACATTTTGTAAAAGGCCATTTCTTTCTTG
3850 3860 3870 3880 3890 3900
22437
1247
GGAGTTTTTTGGTGTGTCTGTTTTTTTAAAGTATTCAAGATACTACCAGTCAACATCTTT
3910 3920 3930 3940 3950 3960
22437
1247
TTGGAAGAAAATGCCTTGGGTTTAGAAGATTTTCTTAAAAGGGGAGTAGATGGTTGTAGA
3970 3980 3990 4000 4010 4020

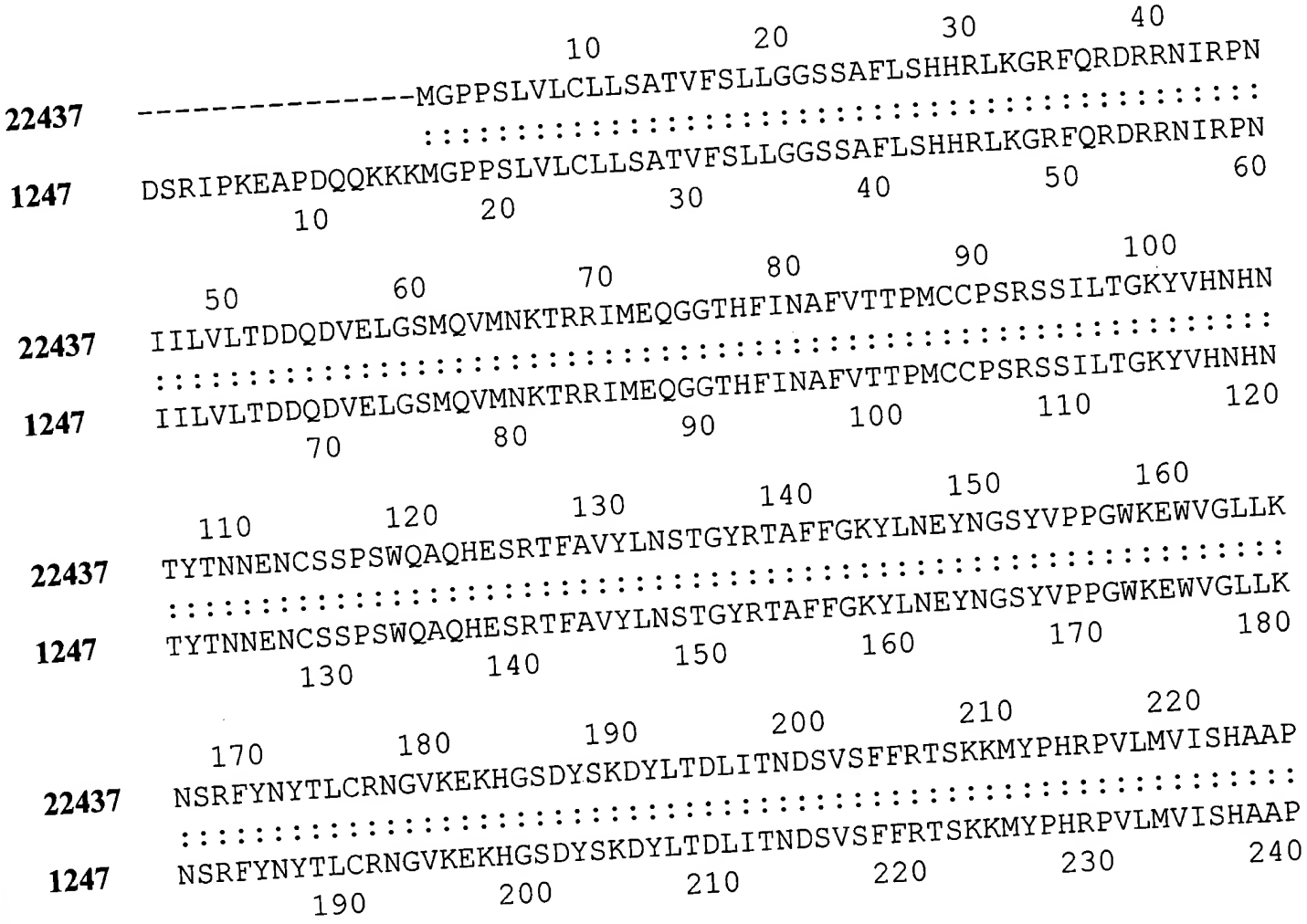
Fig. 3Q

```
22437  ----------------------------------------------------------------

1247   TTGACTAAAAAGTCTACCATACTTCAAGGGACTACAGGTAAGTCTCATAGTATACCAGCT
             4030       4040       4050       4060       4070       4080

22437  ----------------------------------------------------------------

1247   TTGGTACTTCATTTTTTAAAAAAGTATTAATCAATTGCAAAGAAATTCGCCTTGGCCAAC
             4090       4100       4110       4120       4130       4140

22437  ----------------------------------------------------------------

1247   CCTTCTTTGTGTATCAGGTAGTCTAACCTGATACAAGTAGTTGACAGATTTCAACTATCA
             4150       4160       4170       4180       4190       4200

22437  ----------------------------------------------------------------

1247   ATCACCAGTCCAACCCATTTCTCATTTAACAGATGACGGAGATAATCCCTAAAAGCACCC
             4210       4220       4230       4240       4250       4260
```

Fig. 3R

```
22437   ------------------------------------------------------------

1247    ACATTTGTTTCAATGCCCCAAACAGGCCAAGGCTCCCTAGCAACTCCCTAGTGGCGTTTT
              4270        4280        4290        4300        4310        4320

22437   ------------------------------------------------------------

1247    TTAACTTCTCAGAAACTGTTACCATTATTTGAAATAGGCTTCCTTAACCTCCTTTACCCT
              4330        4340        4350        4360        4370        4380

22437   ----------------

1247    TAACCCAACAGGGATTT
              4390
```

Fig. 3S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1247 DSRIPKEAPDQQKKKMGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPN
22437 IILVLTDDQDVELGSMQVMNKTRRIMEQGGTHFINAFVTTPMCCPSRSSILTGKYVHNHN
1247 IILVLTDDQDVELGSMQVMNKTRRIMEQGGTHFINAFVTTPMCCPSRSSILTGKYVHNHN
22437 TYTNNENCSSPSWQAQHESRTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLK
1247 TYTNNENCSSPSWQAQHESRTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLK
22437 NSRFYNYTLCRNGVKEKHGSDYSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAP
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Fig. 4A

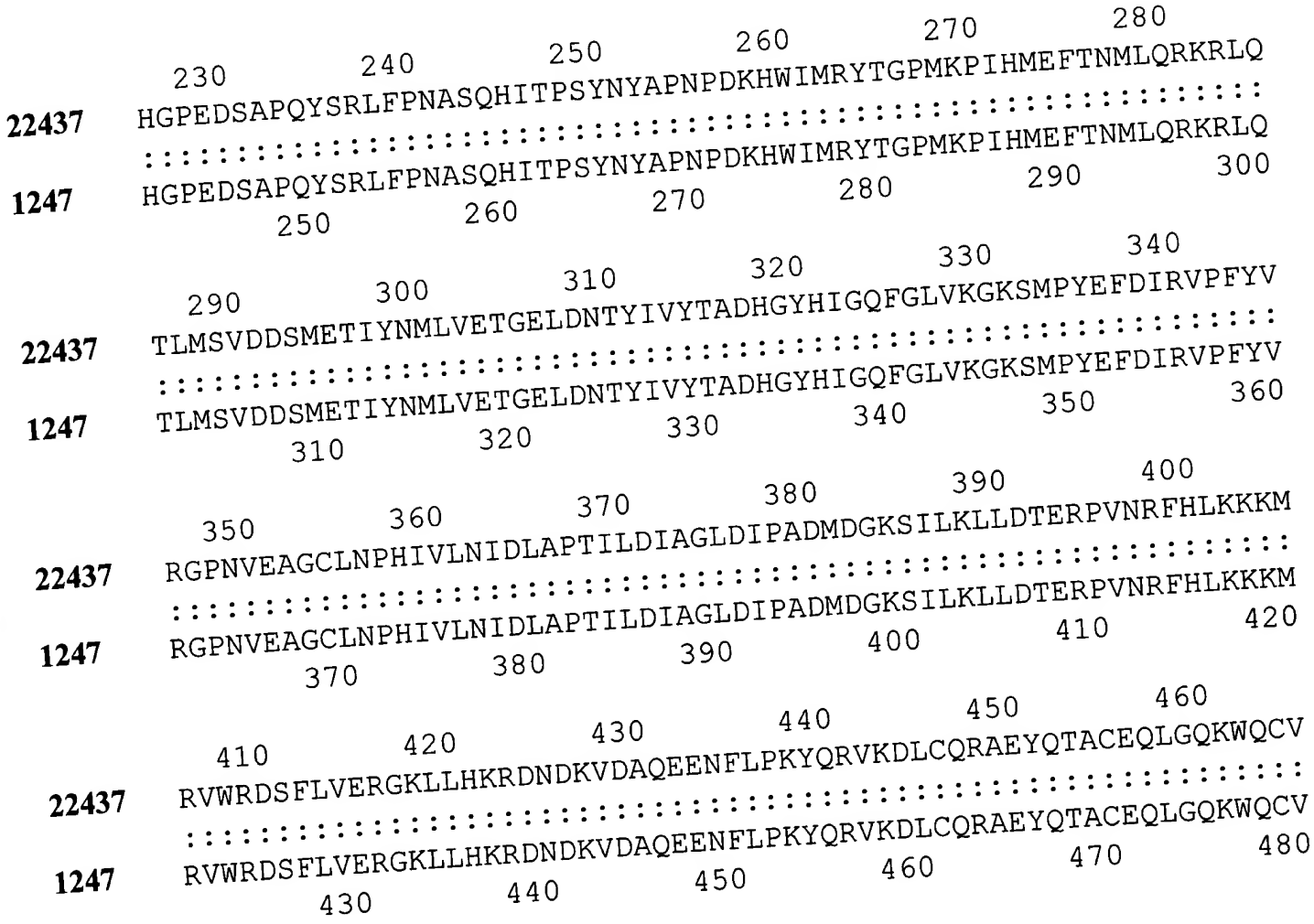
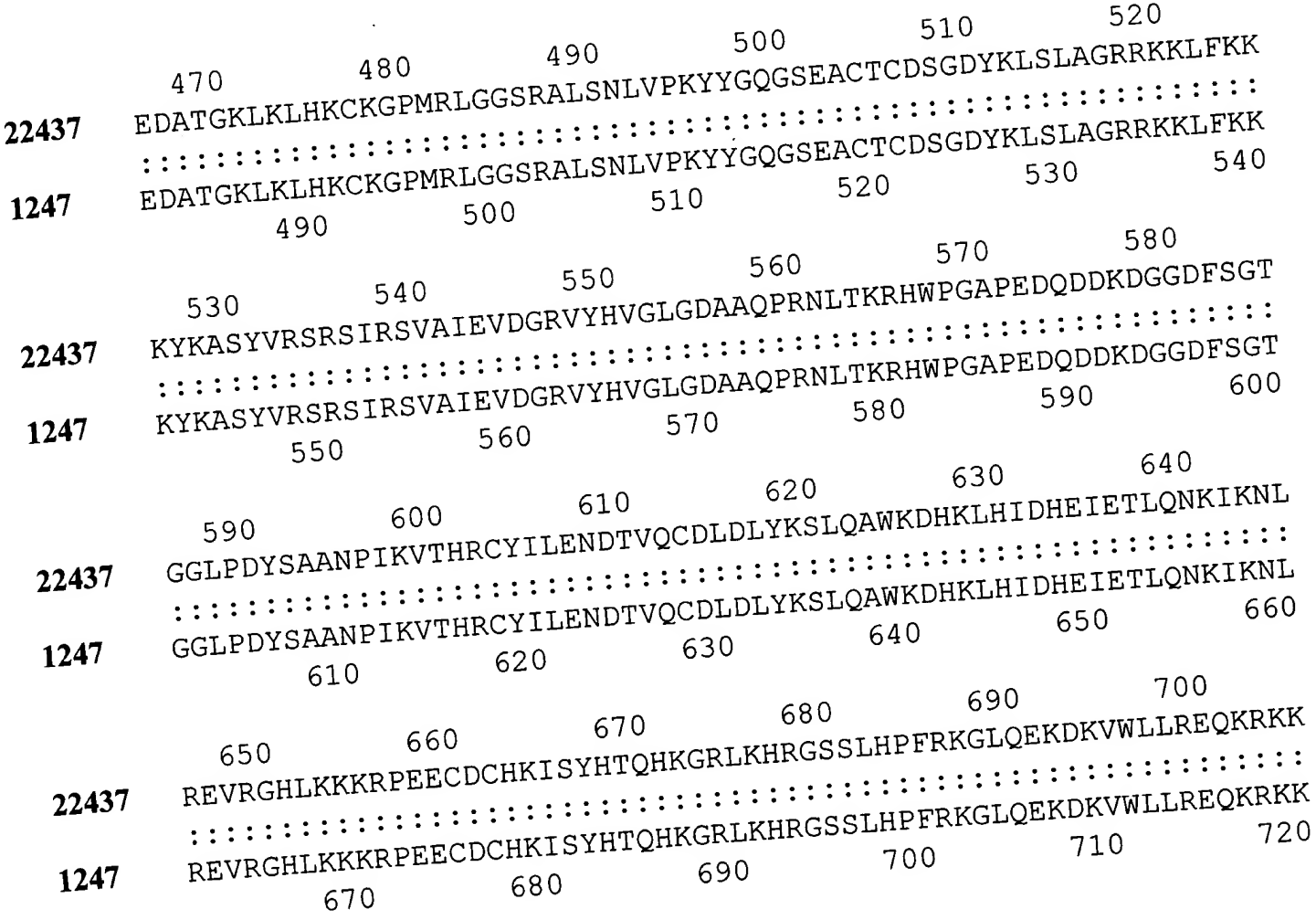

22437 HGPEDSAPQYSRLFPNASQHITPSYNYAPNPDKHWIMRYTGPMKPIHMEFTNMLQRKRLQ
1247 HGPEDSAPQYSRLFPNASQHITPSYNYAPNPDKHWIMRYTGPMKPIHMEFTNMLQRKRLQ
22437 TLMSVDDSMETIYNMLVETGELDNTYIVYTADHGYHIGQFGLVKGKSMPYEFDIRVPFYV
1247 TLMSVDDSMETIYNMLVETGELDNTYIVYTADHGYHIGQFGLVKGKSMPYEFDIRVPFYV
22437 RGPNVEAGCLNPHIVLNIDLAPTILDIAGLDIPADMDGKSILKLLDTERPVNRFHLKKKM
1247 RGPNVEAGCLNPHIVLNIDLAPTILDIAGLDIPADMDGKSILKLLDTERPVNRFHLKKKM
22437 RVWRDSFLVERGKLLHKRDNDKVDAQEENFLPKYQRVKDLCQRAEYQTACEQLGQKWQCV
1247 RVWRDSFLVERGKLLHKRDNDKVDAQEENFLPKYQRVKDLCQRAEYQTACEQLGQKWQCV

Fig. 4B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22437 EDATGKLKLHKCKGPMRLGGSRALSNLVPKYYGQGSEACTCDSGDYKLSLAGRRKKLFKK
1247 EDATGKLKLHKCKGPMRLGGSRALSNLVPKYYGQGSEACTCDSGDYKLSLAGRRKKLFKK
490 500 510 520 530 540
530 540 550 560 570 580
22437 KYKASYVRSRSIRSVAIEVDGRVYHVGLGDAAQPRNLTKRHWPGAPEDQDDKDGGDFSGT
1247 KYKASYVRSRSIRSVAIEVDGRVYHVGLGDAAQPRNLTKRHWPGAPEDQDDKDGGDFSGT
550 560 570 580 590 600
590 600 610 620 630 640
22437 GGLPDYSAANPIKVTHRCYILENDTVQCDLDLYKSLQAWKDHKLHIDHEIETLQNKIKNL
1247 GGLPDYSAANPIKVTHRCYILENDTVQCDLDLYKSLQAWKDHKLHIDHEIETLQNKIKNL
610 620 630 640 650 660
650 660 670 680 690 700
22437 REVRGHLKKKRPEECDCHKISYHTQHKGRLKHRGSSLHPFRKGLQEKDKVWLLREQKRKK
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670 680 690 700 710 720

Fig. 4C

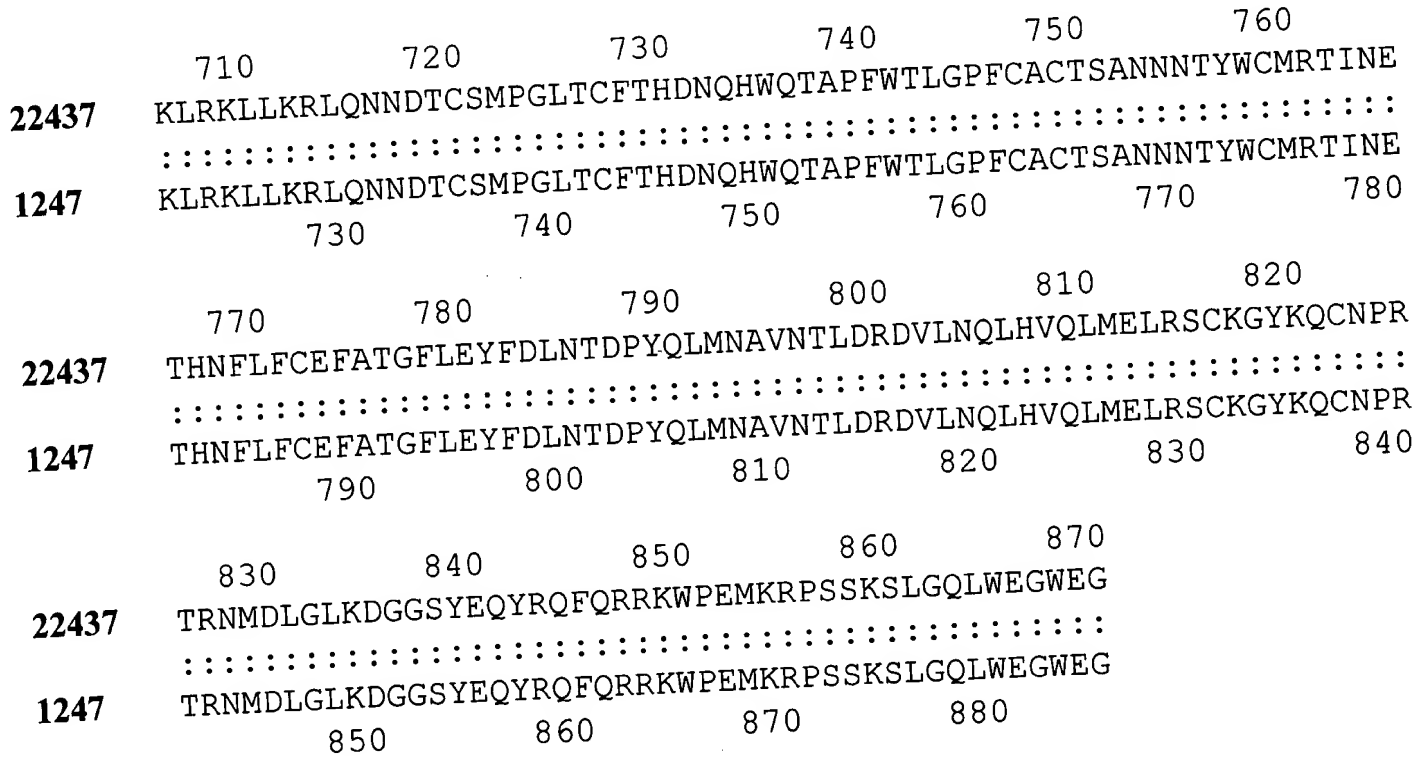

Fig. 4D